

Viral infection and transmission in a large, well-traced outbreak caused by the SARS-CoV-2 Delta variant

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Abstract

The SARS-CoV-2 Delta variant has spread rapidly worldwide. To provide data on its virological profile, we here report the first local transmission of Delta in mainland China. All 167 infections could be traced back to the first index case. Daily sequential PCR testing of quarantined individuals indicated that the viral loads of Delta infections, when they first become PCR-positive, were on average ~1000 times greater compared to lineage A/B infections during the first epidemic wave in China in early 2020, suggesting potentially faster viral replication and greater infectiousness of Delta during early infection. The estimated transmission bottleneck size of the Delta variant was generally narrow, with 1-3 virions in 29 donor-recipient transmission pairs. However, the transmission of minor iSNVs resulted in at least 3 of the 34 substitutions that were identified in the outbreak, highlighting the contribution of intra-host variants to population-level viral diversity during rapid spread. The SARS-CoV-2 Delta variant has spread rapidly worldwide. Here, the authors characterise a single chain of transmission of Delta in China, and find evidence that it is more infectious and replicates faster during early infection compared to early pandemic lineages.